

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 18:50:07 ; Search time 15.665 Seconds
(without alignments)
370.341 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91

Perfect score: 85

Sequence: 1 HSSDYSWRKQVYS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp19808:*

2: Geneseqp19908:*

3: Geneseqp20006:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20038:*

8: Geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 85 | 100.0 | 15 | 4 | AAB82474 Human ext |
| 2 | 85 | 100.0 | 290 | 2 | AAW83329 Human min |
| 3 | 85 | 100.0 | 330 | 4 | AAE12304 Human NPG |
| 4 | 85 | 100.0 | 331 | 2 | AAW23663 Human neu |
| 5 | 85 | 100.0 | 331 | 2 | AAW70589 Adhesion- |
| 6 | 85 | 100.0 | 331 | 2 | AAW83328 Human min |
| 7 | 85 | 100.0 | 331 | 2 | AAW41721 Human PRO |
| 8 | 85 | 100.0 | 331 | 2 | AAW92460 Human NAF |
| 9 | 85 | 100.0 | 331 | 3 | AAW33465 Human PRO |
| 10 | 85 | 100.0 | 331 | 3 | AAW79561 Cancer sp |
| 11 | 85 | 100.0 | 331 | 3 | AAW44277 Human PRO |
| 12 | 85 | 100.0 | 331 | 3 | AAW95349 Human PRO |
| 13 | 85 | 100.0 | 331 | 4 | AAW93266 Human pol |
| 14 | 85 | 100.0 | 331 | 4 | AAW93324 Human pol |
| 15 | 85 | 100.0 | 331 | 4 | AAW38872 Human pol |
| 16 | 85 | 100.0 | 331 | 4 | AAW82472 Human ext |
| 17 | 85 | 100.0 | 331 | 5 | ABG61806 Prostate |
| 18 | 85 | 100.0 | 331 | 5 | AAU79944 Human Spo |
| 19 | 85 | 100.0 | 331 | 5 | ABB77393 Human spo |
| 20 | 85 | 100.0 | 331 | 5 | AAE20463 Human tum |
| 21 | 85 | 100.0 | 331 | 6 | ABO25223 Novel hum |
| 22 | 85 | 100.0 | 331 | 6 | ABU72229 Novel hum |
| 23 | 85 | 100.0 | 331 | 6 | ABU84909 Human sec |
| 24 | 85 | 100.0 | 331 | 6 | ABU61107 Human PRO |
| 25 | 85 | 100.0 | 331 | 6 | ABU80376 Human sec |

| | | | | | |
|----|----|-------|-----|---|--------------------|
| 26 | 85 | 100.0 | 331 | 6 | ABG75949 Human ant |
| 27 | 85 | 100.0 | 331 | 6 | ADA24775 Novel hum |
| 28 | 85 | 100.0 | 331 | 6 | ABO19678 Novel hum |
| 29 | 85 | 100.0 | 331 | 6 | ADA12436 Human sec |
| 30 | 85 | 100.0 | 331 | 6 | ABO19569 Novel hum |
| 31 | 85 | 100.0 | 331 | 7 | ADB73742 Human PRO |
| 32 | 85 | 100.0 | 331 | 7 | ADB76458 Human PRO |
| 33 | 85 | 100.0 | 331 | 7 | ADB75561 Prostate |
| 34 | 85 | 100.0 | 331 | 7 | ADC43884 Human sec |
| 35 | 85 | 100.0 | 331 | 7 | ADC61644 Human sec |
| 36 | 85 | 100.0 | 331 | 7 | ADC63608 Human sec |
| 37 | 85 | 100.0 | 331 | 7 | ADC66708 Human sec |
| 38 | 85 | 100.0 | 331 | 7 | ADC68832 Human sec |
| 39 | 85 | 100.0 | 331 | 7 | ADC62892 Human sec |
| 40 | 85 | 100.0 | 331 | 7 | ADC67957 Human sec |
| 41 | 85 | 100.0 | 331 | 7 | ADC41277 Human sec |
| 42 | 85 | 100.0 | 331 | 7 | ADC67332 Human sec |
| 43 | 85 | 100.0 | 331 | 7 | ADC62268 Human sec |
| 44 | 85 | 100.0 | 331 | 7 | ADC41901 Human sec |
| 45 | 85 | 100.0 | 331 | 7 | ADE49270 Human sec |

ALIGNMENTS

RESULT 1

AAAB82474

ID AAB82474 standard; peptide; 15 AA.

XX AAB82474;

XX 22-AUG-2001 (first entry)

XX Human extracellular matrix protein RGI immunogenic peptide 3C.

XX RGI; human; extracellular matrix protein; prostate cancer; metastasis; tumour; benign prostatic hyperplasia; therapy; diagnosis; antitumour; immunogen.

XX Homo sapiens.

XX WO200144291-A2.

XX 21-JUN-2001.

XX 15-DEC-2000; 2000WO-US033901.

XX 16-DEC-1999; 99US-0172370P.

XX 07-DEC-2000; 2000US-00732357.

XX (SCHD) SCHERING AG.

XX Harkins R, Parkes D, Parry G, Schneider DW, Steinbrecher R;

XX WPI; 2001-398128/42.

XX Novel human extracellular matrix polypeptide, RGI, useful in research, diagnosis and treatment of metastasis such as prostate cancer.

XX Claim 26; Page 48; 69pp; English.

XX The present sequence is that of immunogenic peptide 3C of human RGI (see AAB82472). RGI is a new homologue of the extracellular matrix protein family that is expressed in prostate tissue and which may be over-expressed in prostate tumours. Peptide 3C corresponds to amino acid residues 77-91 of RGI. It was selected as a potential immunogen because of its predicted position at the surface of the protein. Antisera raised against peptide 3C recognise RGI. An antibody that specifically binds to the peptide is claimed. The invention provides human RGI polypeptides, polynucleotides encoding them, and antibodies which specifically bind RGI or a polypeptide such as the present sequence. Such antibodies can be used for diagnosis and/or detection of RGI expression, or can be conjugated (e.g. as an Fv, Fab' or F(ab')2 fragment) to a therapeutic

CC agent, especially a cytotoxic agent, for administration to a patient for
CC treatment of diseases characterised by RGI activity or expression, such
CC as prostate cancer
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 85; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.2e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSMWRKNQYVS 15
| | | | | | | | | | | | | | |
Db 1 HSSDYSMWRKNQYVS 15

RESULT 2
AAW83329
ID AAW83329 standard; protein; 290 AA.
XX
AC AAW83329;
XX
DT 01-MAR-1999 (first entry)
XX
DE Human mindin-related polypeptide.
XX
KW Mindin; human; integrin ligand; angiogenic disease; cancer; metastasis;
KW chronic inflammatory disorder; rheumatoid arthritis; atherosclerosis;
KW macular degeneration, diabetic retinopathy; restenosis;
KW Alzheimer's disease; neural disorder; tissue remodelling; therapy;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO9850073-A1.
XX
PD 12-NOV-1998.
XX
PF 07-MAY-1998; 98WO-US009476.
XX
PR 09-MAY-1997; 97US-0046106P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Jonak ZL, Trulli SH, Tsui P, Lane PA;
XX
DR WPI; 1999-034688/03.
DR N-PSDB; AAV72538.

A new polypeptide is the integrin ligand, human mindin - useful in
therapy and diagnostic assays for diseases such as those associated with
angiogenesis.

Claim 14; Page 30-31; 39pp; English.

This amino acid sequence was deduced from the nucleotide sequence (see
AAV72538) of expressed sequence tags identified prior to the isolation of
a full-length sequence (see AAV72537) encoding human mindin (see
AAW83328). Claimed polypeptides have an amino acid sequence which has at
least 70%, 80%, 90%, 95% or 97-77% identity to this polypeptide, or
comprise the amino acid sequence of the polypeptide itself, or are
encoded by a polynucleotide comprising the sequence contained in
AAV72538. The invention relates to human mindin polypeptides and
polynucleotides (see also AAV72537). Mindin is a novel integrin ligand
suggested to have multifunctional activity in normal and disease states.
Methods are provided for using mindin polypeptides and polynucleotides in
the treatment and diagnosis of angiogenic diseases (cancer, cancer
metastasis, chronic inflammatory disorders, rheumatoid arthritis,
atherosclerosis, macular degeneration, diabetic retinopathy), restenosis,
Alzheimer's disease, neural disorders and tissue remodelling. The
invention also relates to methods for identifying agonists and
antagonists/inhibitors and for treating conditions associated with human
mindin imbalance with the identified compounds. Diagnostic assays for
detecting diseases associated with inappropriate human mindin activity or

CC levels are also claimed
XX
SQ Sequence 290 AA;

Query Match 100.0%; Score 85; DB 2; Length 290;
Best Local Similarity 100.0%; Pred. No. 9.1e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSMWRKNQYVS 15
| | | | | | | | | | | | | | |
Db 77 HSSDYSMWRKNQYVS 91

RESULT 3
AAE12304
ID AAE12304 standard; protein; 330 AA.
XX
AC AAE12304;
XX
DT 03-JAN-2002 (first entry)
XX
DE Human NPG-1 protein.
XX
KW Human; NPG-1; cytostatic; gene therapy; tumour; prostate cancer; LCS;
KW Linker Capture Subtraction; genetic alteration; nerve cell growth.
XX
OS Homo sapiens.
XX
PN US6287777-B1.
XX
PD 11-SEP-2001.
XX
PF 10-AUG-1999; 99US-00371696.
XX
PR 10-MAY-1996; 96US-00644326.
PR 11-FEB-1998; 98US-00022238.
XX
PA (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
XX
PI Sytkowski AJ, Yang M;
XX
DR WPI; 2001-624488/72.
DR N-PSDB; AAD20094.

Detecting the presence of a nucleic acid encoding NPG-1 in a sample
comprises contacting the sample with a nucleic acid probe or primer which
hybridizes under stringent conditions to NPG-1 nucleic acid.

Example; Fig 2; 35pp; English.

The invention relates to a method termed Linker Capture Subtraction (LCS)
for detecting the presence of a nucleic acid encoding NPG-1. NPG-1 gene
is differentially expressed in prostate tumours. The method is used for
identifying nucleic acids encoding NPG-1. NPG-1 can be used for treating
a subject having a tumour, cancer, for the adhesion and outgrowth of
axon, for stimulating growth of nerve cell, and regenerating nerve cells.
The NPG-1 nucleic acid, protein and antibodies may be used in screening
assays, detecting assays, and predictive medicine. The nucleic acids are
further used to express an NPG-1 protein, to detect NPG-1 mRNA or a
genetic alteration in an NPG-1 gene, and to modulate NPG-1 activity. The
present sequence is human NPG-1 protein

XX
SQ Sequence 330 AA;

Query Match 100.0%; Score 85; DB 4; Length 330;
Best Local Similarity 100.0%; Pred. No. 1e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSSDYSMWRKNQYVS 15
| | | | | | | | | | | | | | |
Db 77 HSSDYSMWRKNQYVS 91

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OM protein - protein search, using sw model

Run on: November 14, 2005, 18:59:18 ; Search time 2.88177 Seconds
(without alignments)
500.821 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91

Perfect score: 85

Sequence: 1 HSSDYSMRKNQYVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1 | 46 | 54.1 | 438 | 1 | ALBH |
| 2 | 43.5 | 51.2 | 545 | 2 | T40207 |
| 3 | 42 | 49.4 | 435 | 2 | JC7137 |
| 4 | 42 | 49.4 | 435 | 2 | S12625 |
| 5 | 42 | 49.4 | 729 | 2 | C4854 |
| 6 | 42 | 49.4 | 729 | 2 | H90813 |
| 7 | 42 | 49.4 | 729 | 2 | D85673 |
| 8 | 42 | 49.4 | 1080 | 2 | A71485 |
| 9 | 42 | 49.4 | 3587 | 2 | I40486 |
| 10 | 42 | 49.4 | 3587 | 2 | E97103 |
| 11 | 41 | 48.2 | 121 | 2 | E97103 |
| 12 | 41 | 48.2 | 304 | 2 | D82189 |
| 13 | 41 | 48.2 | 372 | 2 | G89921 |
| 14 | 41 | 48.2 | 410 | 2 | S77661 |
| 15 | 41 | 48.2 | 432 | 2 | G90268 |
| 16 | 41 | 48.2 | 805 | 2 | T34212 |
| 17 | 40 | 47.1 | 135 | 2 | C21826 |
| 18 | 40 | 47.1 | 153 | 2 | A21826 |
| 19 | 40 | 47.1 | 299 | 2 | D82880 |
| 20 | 40 | 47.1 | 337 | 2 | AD3614 |
| 21 | 40 | 47.1 | 423 | 2 | T09942 |
| 22 | 40 | 47.1 | 427 | 1 | ALBHB |
| 23 | 40 | 47.1 | 429 | 1 | J80406 |
| 24 | 40 | 47.1 | 527 | 2 | A82431 |
| 25 | 40 | 47.1 | 836 | 2 | T42323 |
| 26 | 40 | 47.1 | 1179 | 2 | T35093 |
| 27 | 39 | 45.9 | 88 | 2 | A71023 |
| 28 | 39 | 45.9 | 111 | 2 | B25159 |
| 29 | 39 | 45.9 | 279 | 2 | D82243 |

30 39 45.9 379 2 T50967
31 39 45.9 425 2 S68305
32 39 45.9 437 2 JC7138
33 39 45.9 440 2 S14958
34 39 45.9 446 2 H90063
35 39 45.9 494 2 T28660
36 39 45.9 568 2 T28876
37 39 45.9 1085 2 S55352
38 39 45.9 1150 2 T15277
39 38 44.7 69 2 PC1257
40 38 44.7 260 2 T22990
41 38 44.7 261 2 D86729
42 38 44.7 296 2 T12770
43 38 44.7 347 2 T23944
44 38 44.7 393 2 S39383
45 38 44.7 415 2 B84544

ALIGNMENTS

RESULT 1

ALBH
alpha-amylase (EC 3.2.1.1) precursor - barley
C:Species: Hordeum vulgare (barley)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A00846; S65602
R:Rogers, J.C.; Milliman, C.
J. Biol. Chem. 258, 8169-8174, 1983
A:Title: Isolation and sequence analysis of a barley alpha-amylase cDNA clone.
A:Reference number: A00846; MUID:83238423; PMID:6190808
A:Accession: A00846
A:Molecule type: mRNA
A:Residues: 1-438 <ROG>
A:Cross-references: UNIPROT:P00693; GB:J01236; NID:G166986; PID:AAA32929.1; PID:G166987
A:Experimental source: cv. Himalaya
R:Juge, N.; Rodenburg, K.W.; Guo, X.J.; Chaix, J.C.; Svensson, B.
FEBS Lett. 363, 299-303, 1995
A:Title: Isozyme hybrids within the protruding third loop domain of the barley alpha-amylase
A:Reference number: S65602; MUID:95255567; PMID:7737421
A:Accession: S65602
A:Molecule type: protein
A:Residues: 25-29 <JUG>
C:Comment: Production of this enzyme in barley is hormonally regulated. Germinating barley

Query Match

Best Local Similarity 54.1%; Score 46; DB 1; Length 438;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 HSSDYSMRKN 11
DB 419 HGNDYAVWEKN 429

Query Match 54.1%; Score 46; DB 1; Length 438;
Best Local Similarity 54.5%; Pred. No. 9.7;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 2

T40207
hypothetical protein SPBC31F10.04c - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T40207
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21913
A:Accession: T40207

A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-545 <WOO>
A;Cross-references: UNIPROT:P87306; EMBL:Z97204; PIDN:CAB10081.1; GSPDB:GN00067; SPDB:SF
A;Experimental source: strain 972h-; cosmid c31F10
C;Genetics:
A;Gene: SPDB:SPBC31F10.04c
A;Map position: 2
A;Introns: 30/2; 113/2

Query Match 51.2%; Score 43.5; DB 2; Length 545;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

Qy 1 HSSDYSWVR-KNOYVS 15
Db 502 HGTDRKSVWRCKDQYSS 517

RESULT 3
JC7137
alpha-amylase (EC 3.2.1.1) isozyme I - rice
N;Alternate names: 1,4-gulcan glucanohydrolase I
C;Species: Oryza sativa (rice)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
C;Accession: JC7137; PC7039
R;Abe, R.; Yoshida, K.; Aoyagi, M.; Kasahara, S.; Ichishima, E.; Nakajima, T.
Biosci. Biotechnol. Biochem. 63, 1329-1335, 1999
A;Title: Characterization of chimeric enzymes constructed between two distinct alpha-amylase
A;Reference number: JC7137; MUID:99430781; PMID:10500994
A;Accession: JC7137
A;Molecule type: mRNA
A;Residues: 1-435 <AB>
A;Accession: PC7039
A;Molecule type: protein
A;Residues: 245-252 <AB2>
C;Comment: This enzyme catalyzes the hydrolysis of internal alpha-glucosidic linkages in
C;Genetics:
A;Gene: amy-I
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: calcium binding; germination; glycosidase; hydrolase; seed

Query Match 49.4%; Score 42; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRK 10
Db 415 HGKDYSVWEK 424

RESULT 4
SL2625
alpha-amylase (EC 3.2.1.1) 3D - rice
C;Species: Oryza sativa (rice)
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 09-Jul-2004
C;Accession: SL2625; SL2776; S15054; JT0945
R;Huang, N.; Koizumi, N.; Reini, S.; Rodriguez, R.L.
Nucleic Acids Res. 18, 7007-7014, 1990
A;Title: Structural organization and differential expression of rice alpha-amylase genes
A;Reference number: JT0945; MUID:91086278; PMID:2263460
A;Accession: SL2625
A;Molecule type: DNA
A;Residues: 1-435 <HUA>
A;Cross-references: UNIPROT:P27933; EMBL:M59351; NID:G169770; PIDN:AAA33895.1; PID:G1697
R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R.L.
Mol. Gen. Genet. 221, 235-244, 1990
A;Title: The alpha-amylase genes in Oryza sativa: characterization of cDNA clones and mR
A;Reference number: SL2775; MUID:90318322; PMID:2370848
A;Accession: SL2776
A;Molecule type: mRNA
A;Residues: 1-435 <ONE>

A;Cross-references: EMBL:M24287
R;O'Neill, S.D.; Kumagai, M.H.; Majumdar, A.; Huang, N.; Sutcliffe, T.D.; Rodriguez, R.L.
submitted to the EMBL Data Library, April 1989
A;Description: The alpha-amylase genes in Oryza sativa: Characterization of cDNA clones
A;Reference number: S15054
A;Accession: S15054
A;Molecule type: mRNA
A;Residues: 1-72, 'R', '75-136, 'R', '138-435 <ON2>
A;Cross-references: EMBL:M24287; NID:G169754; PIDN:AAA33886.1; PID:G169755
C;Genetics:
A;Introns: 30/3; 342/3
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: wheat alpha-amylase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
R;170-314/Domain: alpha-amylase core homology <AMY>
F;203,228,311/Active site: Asp, Glu, Asp #status predicted

Query Match 49.4%; Score 42; DB 2; Length 435;
Best Local Similarity 60.0%; Pred. No. 42;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HSSDYSWVRK 10
Db 415 HGKDYSVWEK 424

RESULT 5
C64854
ferric-coprogen receptor precursor - Escherichia coli (strain K-12)
N;Alternate names: outer membrane protein fhuE
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: C64854; S09262; A26875; PC4409
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: C64854
A;Accession: C64854
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-729 <BLAT>
A;Cross-references: UNIPROT:P16869; GB:AE000210; GB:U00096; NID:G1787332; PIDN:AAC74186
A;Experimental source: strain K-12, substrain MG1655
R;Sauer, M.; Hantke, K.; Braun, V.
Mol. Microbiol. 4, 427-437, 1990
A;Title: Sequence of the fhuE outer-membrane receptor gene of Escherichia coli K12 and p
A;Reference number: S09262; MUID:90286919; PMID:2162465
A;Accession: S09262
A;Molecule type: DNA
A;Residues: 1-362, 'C', '364-729 <SAU>
A;Cross-references: EMBL:X17615; NID:G41448; PIDN:CAA35616.1; PID:G41449
A;Experimental source: strain K-12
R;Sauer, M.; Hantke, K.; Braun, V.
J. Bacteriol. 169, 2044-2049, 1987
A;Title: Ferric-coprogen receptor FhuE of Escherichia coli: processing and sequence comm
A;Reference number: A26875; MUID:87194585; PMID:3032906
A;Accession: A26875
A;Molecule type: DNA
A;Residues: 1-69 <SA2>
R;Kobayashi, Y.; Sasamura, A.; Nishimura, A.; Kuratomi, K.
Res. Commun. Biochem. Cell Mol. Biol. 1, 157-170, 1997
A;Title: A novel 14-kilodalton protein in P1,P4-bis(S'-adenosyl)tetrathosphate (AP4A)-ba
A;Reference number: JC5685
A;Accession: PC4409
A;Molecule type: DNA
A;Residues: 1-47 <KOB>
C;Genetics:
A;Gene: fhuE
A;Map position: 16 min
C;Function:

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OM protein - protein search, using sw model

Run on: November 14, 2005, 18:51:02 ; Search time 14.0025 Seconds
(without alignments)
548.560 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91

Perfect score: 85

Sequence: 1 HSSDYSWKRKNQYVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_crenbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|--------------|---------------------|
| 1 | 85 | 100.0 | 331 | 1 SPO2 HUMAN | Q9bude6 homo sapien |
| 2 | 82 | 96.5 | 289 | 2 Q8KA56 | Q8ka56 mus musculus |
| 3 | 82 | 96.5 | 330 | 1 SPO2 MOUSE | Q8bms2 mus musculus |
| 4 | 82 | 96.5 | 330 | 1 SPO2 RAT | Q9wv75 rattus norv |
| 5 | 82 | 96.5 | 330 | 2 Q8VD28 | Q8vd28 mus musculus |
| 6 | 63 | 74.1 | 331 | 2 Q42112 | Q42112 brachydanio |
| 7 | 55 | 64.7 | 313 | 2 Q8DCW4 | Q8dcm4 xenopus lae |
| 8 | 49 | 57.6 | 138 | 2 Q82UD3 | Q82ud3 nitrosomona |
| 9 | 49 | 57.6 | 420 | 2 Q22019 | Q22019 cyanidiosch |
| 10 | 49 | 57.6 | 446 | 2 Q85G84 | Q85g84 cyanidiosch |
| 11 | 47 | 55.3 | 390 | 2 Q7Y4U7 | Q7y4u7 bacterioph |
| 12 | 46 | 54.1 | 438 | 1 AMV1 HORVU | P00693 hordeum vul |
| 13 | 46 | 54.1 | 438 | 2 Q40017 | Q40017 hordeum vul |
| 14 | 46 | 54.1 | 1453 | 2 Q75SD1 | Q75sd1 ashbya goss |
| 15 | 45 | 52.9 | 845 | 2 Q9GR11 | Q9gr11 leishmania |
| 16 | 44 | 51.8 | 434 | 2 Q81699 | Q81699 avena fatua |
| 17 | 44 | 51.8 | 434 | 2 Q87CW9 | Q87cw9 xylella fas |
| 18 | 44 | 51.8 | 437 | 2 Q81700 | Q81700 avena fatua |
| 19 | 44 | 51.8 | 839 | 2 Q8ML26 | Q8ml26 drosophila |
| 20 | 44 | 51.8 | 3099 | 2 Q7R514 | Q7r514 gardia lam |
| 21 | 43.5 | 51.2 | 545 | 1 SBB4 SCHPO | P87306 schizosacch |
| 22 | 43.5 | 51.2 | 570 | 2 Q8D4R4 | Q8d4r4 vibrio vuln |
| 23 | 43.5 | 51.2 | 602 | 2 Q7MGB8 | Q7mgb8 vibrio vuln |
| 24 | 43 | 50.6 | 273 | 1 HTS6 METAC | Q8tt96 methanoearc |
| 25 | 43 | 50.6 | 463 | 2 Q89K78 | Q89kw8 bradyrhizob |
| 26 | 43 | 50.6 | 809 | 2 Q7NAF2 | Q7naf2 mycoplasma |
| 27 | 42 | 49.4 | 92 | 2 Q6DC15 | Q6dc15 brachydanio |
| 28 | 42 | 49.4 | 105 | 2 Q73915 | Q73915 bacillus ce |
| 29 | 42 | 49.4 | 206 | 2 Q99L35 | Q99l35 mus musculus |
| 30 | 42 | 49.4 | 230 | 2 Q7T5M1 | Q7t5m1 cryptophleb |
| 31 | 42 | 49.4 | 239 | 2 Q8JR20 | Q8jr20 pthoriramae |

RESULT 1

| ID | SPO2_HUMAN | STANDARD; | PRT; | 331 AA. |
|----|---|-----------|------|---------|
| AC | Q9BUD6; Q9ULW1; | | | |
| DT | 25-OCT-2004 (Rel. 45, Created) | | | |
| DT | 25-OCT-2004 (Rel. 45, Last sequence update) | | | |
| DT | 25-JAN-2005 (Rel. 46, Last annotation update) | | | |
| DE | Spondin 2 precursor (Madin) (Differentially expressed in cancerous and noncancerous lung cells 1) (DIL-1) (UNQ435/PRO866). | | | |
| GN | Name=SPON2; Synonyms=DIL1; | | | |
| OS | Homo sapiens (Human). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | |
| OX | NCBI_TaxID=9606; | | | |
| RV | [1] | | | |
| RP | SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANTS ALA-122 AND VAL-242. | | | |
| RP | MEDLINE=99443867; PubMed=10512675; DOI=10.1006/geno.1999.5939; | | | |
| RA | Manda R., Kohno T., Matsuno Y., Takenoshita S., Kuwano H., Yokota J.; | | | |
| RT | "Identification of genes (SPON2 and C20orf2) differentially expressed between cancerous and noncancerous lung cells by mRNA differential display."; | | | |
| RT | Genomics 61:5-14(1999). | | | |
| RL | [2] | | | |
| RV | SEQUENCE FROM N.A. | | | |
| RP | MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; | | | |
| RA | Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., | | | |
| RA | Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., | | | |
| RA | Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., | | | |
| RA | Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., | | | |
| RA | Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., | | | |
| RA | Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., | | | |
| RA | Vandlen R., Watanabe C., Wiedand D., Woods K., Xie M.-H., Yansura D., | | | |
| RA | Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., | | | |
| RA | Godowski P., Gray A.; | | | |
| RT | "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment."; | | | |
| RT | Genome Res. 13:2265-2270(2003). | | | |
| RL | [3] | | | |
| RV | SEQUENCE FROM N.A., AND VARIANTS ALA-122 AND VAL-242. | | | |
| RP | PubMed=14702039; DOI=10.1038/ng1285; | | | |
| RA | Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R., | | | |
| RA | Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H., | | | |
| RA | Sekine M., Ohayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., | | | |
| RA | Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., | | | |
| RA | Nagahori K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., | | | |
| RA | Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., | | | |
| RA | Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., | | | |
| RA | Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., | | | |
| RA | Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., | | | |
| RA | Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., | | | |
| RA | Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., | | | |
| RA | Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O., | | | |

ALIGNMENTS

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 19:00:53 ; Search time 4.10099 Seconds
(without alignments)
273.041 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91

Perfect score: 85

Sequence: 1 HSSDYSWMRKXQYVS 15

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 2 | 85 | 100.0 | 330 | 3 | US-09-371-696-2 |
| 3 | 85 | 100.0 | 331 | 2 | US-08-799-173A-2 |
| 4 | 85 | 100.0 | 331 | 4 | US-09-732-357B-2 |
| 5 | 85 | 100.0 | 331 | 4 | US-09-170-042A-2 |
| 6 | 82 | 96.5 | 330 | 4 | US-09-732-357B-13 |
| 7 | 52 | 61.2 | 299 | 4 | US-09-311-021-202 |
| 8 | 44 | 51.8 | 677 | 4 | US-09-270-767-58094 |
| 9 | 44 | 51.8 | 847 | 4 | US-09-270-767-42783 |
| 10 | 42 | 49.4 | 25 | 4 | US-09-270-767-58735 |
| 11 | 42 | 49.4 | 250 | 4 | US-09-248-796A-15562 |
| 12 | 42 | 49.4 | 435 | 3 | US-09-072-917A-9 |
| 13 | 42 | 49.4 | 877 | 4 | US-09-165-396-5 |
| 14 | 41 | 48.2 | 149 | 4 | US-09-270-767-47885 |
| 15 | 41 | 48.2 | 297 | 4 | US-09-248-796A-25364 |
| 16 | 40 | 47.1 | 111 | 4 | US-09-248-796A-21330 |
| 17 | 40 | 47.1 | 114 | 4 | US-09-513-999C-5768 |
| 18 | 40 | 47.1 | 456 | 4 | US-09-489-039A-8101 |
| 19 | 40 | 47.1 | 462 | 4 | US-09-543-681A-5290 |
| 20 | 40 | 47.1 | 742 | 4 | US-09-500-123-12 |
| 21 | 40 | 47.1 | 811 | 4 | US-09-500-123-9 |
| 22 | 40 | 47.1 | 871 | 4 | US-09-500-123-7 |
| 23 | 40 | 47.1 | 1008 | 4 | US-09-949-016-10423 |
| 24 | 39 | 45.9 | 152 | 4 | US-09-270-767-37205 |
| 25 | 39 | 45.9 | 152 | 4 | US-09-270-767-52422 |
| 26 | 39 | 45.9 | 163 | 4 | US-09-328-352-7800 |
| 27 | 39 | 45.9 | 249 | 4 | US-09-270-767-43254 |

28 39 45.9 281 4 US-09-248-796A-23359 Sequence 23359, A
29 39 45.9 635 4 US-09-248-796A-16944 Sequence 16944, A
30 39 45.9 1085 1 US-08-431-080-28 Sequence 28, Appl
31 39 45.9 1085 2 US-08-938-534-28 Sequence 28, Appl
32 39 45.9 1085 3 US-09-345-294-28 Sequence 28, Appl
33 39 45.9 1169 1 US-08-542-921-2 Sequence 2, Appl
34 39 45.9 1169 2 US-08-880-685-2 Sequence 2, Appl
35 39 45.9 1169 2 US-08-880-684-2 Sequence 2, Appl
36 38.5 45.3 404 4 US-09-248-796A-19544 Sequence 19544, A
37 38 44.7 126 4 US-09-755-665-27 Sequence 27, Appl
38 38 44.7 133 4 US-09-755-665-4 Sequence 4, Appl
39 38 44.7 172 4 US-08-737-109-17 Sequence 17, Appl
40 38 44.7 185 4 US-09-248-796A-14213 Sequence 14213, A
41 38 44.7 319 4 US-09-107-532A-6215 Sequence 6215, Ap
42 38 44.7 321 3 US-08-915-795-9 Sequence 9, Appl
43 38 44.7 321 4 US-09-847-524-4 Sequence 4, Appl
44 38 44.7 321 4 US-09-296-275-9 Sequence 9, Appl
45 38 44.7 325 3 US-08-915-795-3 Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-09-732-357B-10
; Sequence 10, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357B-10

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Best Local Similarity 100.0%; Pred. No. 1.8e-07;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWMRKXQYVS 15
Db 1 HSSDYSWMRKXQYVS 15

RESULT 2
US-09-371-696-2
; Sequence 2, Application US/09371696
; Patent No. 6287777
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Yang, Meiheng
; TITLE OF INVENTION: NOVEL NPG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE
; FILE REFERENCE: 01948/053002
; CURRENT APPLICATION NUMBER: US/09/371,696
; CURRENT FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: US 09/022,238
; EARLIER FILING DATE: 1998-02-11
; EARLIER APPLICATION NUMBER: US 08/644,326
; EARLIER FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-371-696-2

Query Match 100.0%; Score 85; DB 3; Length 330;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMMRKQYVS 15
Db 77 HSSDYSMMRKQYVS 91

RESULT 3
US-08-799-173A-2
; Sequence 2, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/799,173A
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-799-173A-2

Query Match 100.0%; Score 85; DB 2; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMMRKQYVS 15
Db 77 HSSDYSMMRKQYVS 91

RESULT 4
US-09-732-357B-2
; Sequence 2, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon

; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357B-2

Query Match 100.0%; Score 85; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMMRKQYVS 15
Db 77 HSSDYSMMRKQYVS 91

RESULT 5
US-09-170-042A-2
; Sequence 2, Application US/09170042A
; Patent No. 6759512
; GENERAL INFORMATION:
; APPLICANT: Hastings, Gregg
; APPLICANT: Dillon, Patrick
; TITLE OF INVENTION: Human Neuronal Attachment Factor-1
; FILE REFERENCE: PF226D1
; CURRENT APPLICATION NUMBER: US/09/170,042A
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-170-042A-2

Query Match 100.0%; Score 85; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSMMRKQYVS 15
Db 77 HSSDYSMMRKQYVS 91

RESULT 6
US-09-732-357B-13
; Sequence 13, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 330

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 19:11:14 ; Search time 14.3719 Seconds
(without alignments)
436.695 Million cell updates/sec

Title: US-10-616-279-2_COPY_77_91

Perfect score: 85

Sequence: 1 HSSDYSWRRKNQYVS 15

Scoring table: BLOSUM62

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Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3 | 85 | 100.0 | 15 | 16 | US-10-624-884-10 |
| 4 | 85 | 100.0 | 15 | 17 | US-10-895-183-10 |
| 5 | 85 | 100.0 | 290 | 15 | US-10-829-952-4 |
| 6 | 85 | 100.0 | 330 | 9 | US-09-903-383-2 |
| 7 | 85 | 100.0 | 331 | 9 | US-09-732-357A-2 |
| 8 | 85 | 100.0 | 331 | 9 | US-09-978-295A-236 |
| 9 | 85 | 100.0 | 331 | 9 | US-09-938-418-8 |
| 10 | 85 | 100.0 | 331 | 9 | US-09-978-697-236 |
| 11 | 85 | 100.0 | 331 | 9 | US-09-978-192A-236 |

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| 33 | 85 | 100.0 | 331 | 10 | US-09-978-681A-236 | Sequence 236, App |
| 34 | 85 | 100.0 | 331 | 10 | US-09-978-194A-236 | Sequence 236, App |
| 35 | 85 | 100.0 | 331 | 10 | US-09-999-829A-236 | Sequence 236, App |
| 36 | 85 | 100.0 | 331 | 10 | US-09-978-299A-236 | Sequence 236, App |
| 37 | 85 | 100.0 | 331 | 10 | US-09-978-544A-236 | Sequence 236, App |
| 38 | 85 | 100.0 | 331 | 10 | US-09-978-665A-236 | Sequence 236, App |
| 39 | 85 | 100.0 | 331 | 10 | US-09-978-802A-236 | Sequence 236, App |
| 40 | 85 | 100.0 | 331 | 10 | US-09-970-944-12 | Sequence 12, Appl |
| 41 | 85 | 100.0 | 331 | 10 | US-09-970-944-38 | Sequence 38, Appl |
| 42 | 85 | 100.0 | 331 | 10 | US-09-970-944-39 | Sequence 39, Appl |
| 43 | 85 | 100.0 | 331 | 10 | US-09-970-944-40 | Sequence 40, Appl |
| 44 | 85 | 100.0 | 331 | 11 | US-09-999-831A-236 | Sequence 236, App |
| 45 | 85 | 100.0 | 331 | 12 | US-09-978-824-236 | Sequence 236, App |

ALIGNMENTS

RESULT 1

US-09-732-357A-10
; Sequence 10, Application US/09732357A
; Patent No. US20020004047A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732.357A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357A-10

Query Match 100.0%; Score 85; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HSSDYSWRRKNQYVS 15

Db 1 HSSDYSWRRKNQYVS 15

RESULT 2

```
US-10-616-279-10
; Sequence 10, Application US/10616279
; Publication No. US20040023307A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a Novel US20040023307A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUS1
; CURRENT APPLICATION NUMBER: US/10/616,279
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-279-10

Query Match      100.0%; Score 85; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSSDYSMMRKQYVS 15
Db      1 HSSDYSMMRKQYVS 15
|||||

RESULT 3
US-10-624-884-10
; Sequence 10, Application US/10624884
; Publication No. US20040152139A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; TITLE OF INVENTION: DNA Encoding a Novel RG-1 Polypeptide
; FILE REFERENCE: 51791AUS1
; CURRENT APPLICATION NUMBER: US/10/624,884
; PRIOR FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-624-884-10

Query Match      100.0%; Score 85; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSSDYSMMRKQYVS 15
Db      1 HSSDYSMMRKQYVS 15
|||||

RESULT 4
US-10-895-183-10
; Sequence 10, Application US/10895183
; Publication No. US20050019845A1
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```
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: RG1 Antibodies and Uses Thereof
; FILE REFERENCE: 51791BUSM1
; CURRENT APPLICATION NUMBER: US/10/895,183
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/489,032
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-895-183-10

Query Match      100.0%; Score 85; DB 17; Length 15;
Best Local Similarity 100.0%; Pred. No. 6e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSSDYSMMRKQYVS 15
Db      1 HSSDYSMMRKQYVS 15
|||||

RESULT 5
US-10-629-952-4
; Sequence 4, Application US/10629952
; Publication No. US2004007227A1
; GENERAL INFORMATION:
; APPLICANT: Jonak, Zdenka L
; APPLICANT: Trulli, Stephen H
; APPLICANT: Tsui, Ping
; APPLICANT: Lane, Pamela A.
; TITLE OF INVENTION: INTEGRIN LIGAND, HUMAN MINDIN
; FILE REFERENCE: DDX-100US
; CURRENT APPLICATION NUMBER: US/10/629,952
; CURRENT FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 290
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-629-952-4

Query Match      100.0%; Score 85; DB 15; Length 290;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 HSSDYSMMRKQYVS 15
Db      77 HSSDYSMMRKQYVS 91
|||||

RESULT 6
US-09-903-383-2
; Sequence 2, Application US/09903383
; Patent No. US20020137135A1
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Yang, Weiheng
; TITLE OF INVENTION: NOVEL NPG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE
; TITLE OF INVENTION: TUMORS
; FILE REFERENCE: 01948/053002
; CURRENT APPLICATION NUMBER: US/09/903,383
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/371,696
; PRIOR FILING DATE: 1999-08-10
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 18:50:07 ; Search time 345.675 Seconds
(without alignments)
370.341 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
Sequence: 1 MENPSPAAALGKALCALLA.....NGSPCPLEBEEARCVDPNCV 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Genesep_16Dec04:*
1: Genesep1980s:*
2: Genesep1990s:*
3: Genesep2000s:*
4: Genesep2001s:*
5: Genesep2002s:*
6: Genesep2003as:*
7: Genesep2003bs:*
8: Genesep2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|--------------------|
| 1 | 1760 | 100.0 | 331 | 4 | AAB82472 Human ext |
| 2 | 1752 | 99.5 | 331 | 4 | AAM93324 Human pol |
| 3 | 1752 | 99.5 | 331 | 5 | ABG61806 Prostate |
| 4 | 1752 | 99.5 | 331 | 5 | Aau79944 Human spo |
| 5 | 1752 | 99.5 | 331 | 5 | Abb77393 Human spo |
| 6 | 1752 | 99.5 | 331 | 7 | ADB75561 Prostate |
| 7 | 1752 | 99.5 | 331 | 7 | ADG42585 Human ext |
| 8 | 1752 | 99.5 | 331 | 7 | ADN38814 Cancer/an |
| 9 | 1752 | 99.5 | 331 | 7 | ADN39877 Cancer/an |
| 10 | 1752 | 99.5 | 331 | 8 | ADJ75655 Marker ge |
| 11 | 1752 | 99.5 | 331 | 8 | ADL30814 Human pro |
| 12 | 1752 | 99.5 | 331 | 8 | ADO20071 Human pro |
| 13 | 1752 | 99.5 | 331 | 8 | ADQ18813 Human sof |
| 14 | 1752 | 99.5 | 422 | 8 | ADR66362 Human pro |
| 15 | 1752 | 99.5 | 422 | 8 | ADR66704 Human pro |
| 16 | 1749 | 99.4 | 331 | 4 | AAM38872 Human pol |
| 17 | 1749 | 99.4 | 444 | 4 | AAM40658 Human pol |
| 18 | 1747 | 99.3 | 331 | 3 | AAY79561 Cancer sp |
| 19 | 1744 | 99.1 | 331 | 2 | AAY70589 Adhesion |
| 20 | 1744 | 99.1 | 331 | 2 | AAY41721 Human PRO |
| 21 | 1744 | 99.1 | 331 | 3 | AAB33465 Human PRO |
| 22 | 1744 | 99.1 | 331 | 3 | AAB44277 Human PRO |
| 23 | 1744 | 99.1 | 331 | 3 | AAY95349 Human PRO |
| 24 | 1744 | 99.1 | 331 | 4 | AAM93266 Human pol |
| 25 | 1744 | 99.1 | 331 | 5 | AAB20463 Human tum |

| | | | | | | |
|----|------|------|-----|---|----------|-----------|
| 26 | 1744 | 99.1 | 331 | 6 | ABO25223 | Novel hum |
| 27 | 1744 | 99.1 | 331 | 6 | ABU72229 | Novel hum |
| 28 | 1744 | 99.1 | 331 | 6 | ABU84909 | Human sec |
| 29 | 1744 | 99.1 | 331 | 6 | ABU61107 | Human PRO |
| 30 | 1744 | 99.1 | 331 | 6 | ABU80376 | Human sec |
| 31 | 1744 | 99.1 | 331 | 6 | ABG75949 | Human ant |
| 32 | 1744 | 99.1 | 331 | 6 | ADA24775 | Novel hum |
| 33 | 1744 | 99.1 | 331 | 6 | ABO19678 | Novel hum |
| 34 | 1744 | 99.1 | 331 | 6 | ADA12436 | Human sec |
| 35 | 1744 | 99.1 | 331 | 6 | ABO19569 | Novel hum |
| 36 | 1744 | 99.1 | 331 | 7 | ADB73742 | Human PRO |
| 37 | 1744 | 99.1 | 331 | 7 | ADB76458 | Human PRO |
| 38 | 1744 | 99.1 | 331 | 7 | ADC43884 | Human sec |
| 39 | 1744 | 99.1 | 331 | 7 | ADC61644 | Human sec |
| 40 | 1744 | 99.1 | 331 | 7 | ADC83608 | Human sec |
| 41 | 1744 | 99.1 | 331 | 7 | ADC66708 | Human sec |
| 42 | 1744 | 99.1 | 331 | 7 | ADC68832 | Human sec |
| 43 | 1744 | 99.1 | 331 | 7 | ADC62892 | Human sec |
| 44 | 1744 | 99.1 | 331 | 7 | ADC67957 | Human sec |
| 45 | 1744 | 99.1 | 331 | 7 | ADC41277 | Human sec |

ALIGNMENTS

RESULT 1
AAB82472
ID AAB82472 standard; protein; 331 AA.
XX
AC AAB82472;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human extracellular matrix protein RG1.
XX
KW RG1; human; extracellular matrix protein; prostate cancer; metastasis;
KW tumour; benign prostatic hyperplasia; therapy; diagnosis; antitumour.
XX
OS Homo sapiens.

Key Location/Qualifiers
FH Peptide 28..46
FT /label= Immunogenic_peptide
FT /note= "specifically claimed in claim 25"
FT Domain 31..103
FT /label= F-spondin_domain
FT Peptide 77..91
FT /label= Immunogenic_peptide
FT /note= "specifically claimed in claim 26"
FT Domain 139..221
FT /label= F-spondin_domain
FT Peptide 188..210
FT /label= Immunogenic_peptide
FT /note= "specifically claimed in claim 27"
FT Peptide 263..274
FT /label= Immunogenic_peptide
FT /note= "specifically claimed in claim 28"
FT Domain 278..300
FT /label= Thrombospondin_domain
WO200144291-A2.

21-JUN-2001.
15-DEC-2000; 2000WO-US033901.
16-DEC-1999; 99US-0172370P.
07-DEC-2000; 2000US-00732357.
(SCHD) SCHERING AG.
Harkins R, Parkes D, Parry G, Schneider DW, Steinbrecher R;
XX

DR WPI, 2001-398128/42.
DR N-PSDB; AAF90566, AAF90567.
XX Novel human extracellular matrix polypeptide, RG1, useful in research,
PT diagnosis and treatment of metastasis such as prostate cancer.
XX
PS Claim 1; Fig 2; 69pp; English.
XX
CC The present sequence is that of human RG1, a new homologue of the
CC extracellular matrix protein family, which is expressed in prostate
CC tissue and may be over-expressed in prostate tumours. It shows homology
CC to mindin and f-spondin proteins. This protein family is distinguished by
CC 2 conserved spondin domains near the N-terminus and at least 1
CC thrombospondin type 1 repeat at the C-terminus. The rg1 gene (see
CC AAF90566) was isolated from a database screening. The invention provides
CC human RG polypeptides (especially corresponding to amino acids 1-331, 21-
CC 331, 27-331, 28-46 and 77-91 of RG1), polynucleotides encoding them,
CC methods for producing the polypeptides, expression vectors, genetically
CC engineered host cells for expression of the polypeptides, and antibodies
CC which specifically bind RG1 or its immunologically active fragment
CC (especially a polypeptide comprising amino acid 28-46, 77-91, 188-210, or
CC 263-274 of RG1). It also provides methods for utilizing the
CC polynucleotides, polypeptides and antibodies in research, diagnosis and
CC therapeutic applications. Thus, the antibodies can be used for diagnosis
CC and/or detection of RG1 expression, or can be conjugated to a therapeutic
CC agent, such as a cytotoxic agent, for administration to patient for
CC treatment of diseases characterised by RG1 activity or expression, such
CC as prostate cancer

XX Sequence 331 AA;

Query Match 100.0%; Score 1760; DB 4; Length 331;
Best Local Similarity 100.0%; Pred. No. 4.2e-162;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENPSAAALGKALCALLLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSQTAPPKQY 60
DB 1 MENPSAAALGKALCALLLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSQTAPPKQY 60
QY 61 PLFRPPAQWSSLGAAHSSDYSMWRKNQVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
DB 61 PLFRPPAQWSSLGAAHSSDYSMWRKNQVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
QY 121 HAVFSAVAPVSGTGQTSAELEVRHSLVSFVVRIVPSPDWFVGVDSLDLDCGDRWREQA 180
DB 121 HAVFSAVAPVSGTGQTSAELEVRHSLVSFVVRIVPSPDWFVGVDSLDLDCGDRWREQA 180
QY 181 ALDLYPYDAGTDSGFTFSSPNFATIPQDTVTITSSPSHPANSFYYPRLKALPPIARVT 240
DB 181 ALDLYPYDAGTDSGFTFSSPNFATIPQDTVTITSSPSHPANSFYYPRLKALPPIARVT 240
QY 241 LVRLRQSPRAFIIPAPVLPSPRDNIEIVDSASVPETPLDCEVLSWSSWGLCGGHCRLGTSK 300
DB 241 LVRLRQSPRAFIIPAPVLPSPRDNIEIVDSASVPETPLDCEVLSWSSWGLCGGHCRLGTSK 300
QY 301 RTRVVRVQPNANGSPCPELEEEAECPDNCV 331
DB 301 RTRVVRVQPNANGSPCPELEEEAECPDNCV 331

RESULT 2

AAM93324

ID AAM93324 standard; protein; 331 AA.

XX AAM93324;

XX AAM93324;

DT 06-NOV-2001 (first entry)

DE Human polypeptide, SEQ ID NO: 2847.

XX Human; full length cDNA; cDNA synthesis; oligo-capping.

KW Homo sapiens.

OS

XX EPI130094-A2.
XX
XX 05-SEP-2001.
XX
XX 07-JUL-2000; 2000EP-00114089.
XX
XX 08-JUL-1999; 99JP-00194486.
XX 11-JAN-2000; 2000JP-00118774.
XX 02-MAY-2000; 2000JP-00183765.
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;
XX Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;
XX WPI; 2001-524255/58.
XX N-PSDB; AAK94244.
XX
XX 830 Primers useful for synthesizing full length cDNA clones and their use
XX in genetic manipulation.
XX
XX Claim 8; SEQ ID NO 2847; 1380pp + Sequence Listing; English.

XX The invention relates to primers for synthesising full length cDNA
XX clones. 830 cDNA molecules encoding a human protein have been isolated
XX and nucleotide sequences of 5' - and 3' -ends of the cDNA molecules have
XX been determined. Primers for synthesising the full length cDNA are useful
XX for clarifying the function of the protein encoded by the cDNA. The full
XX length clones were obtained by construction of full length enriched cDNA
XX libraries that were synthesised by the oligo-capping method. The primers
XX enable the production of the full length cDNA easily without any special
XX methods. The present sequence is a polypeptide encoded by a full length
XX human cDNA of the invention. Note: The sequence data for this patent did
XX not form part of the printed specification, but was obtained in CD-ROM
XX format directly from EPO

XX Sequence 331 AA;

Query Match 99.5%; Score 1752; DB 4; Length 331;
Best Local Similarity 99.7%; Pred. No. 2.5e-161;
Matches 330; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MENPSAAALGKALCALLLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSQTAPPKQY 60
DB 1 MENPSAAALGKALCALLLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSQTAPPKQY 60
QY 61 PLFRPPAQWSSLGAAHSSDYSMWRKNQVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
DB 61 PLFRPPAQWSSLGAAHSSDYSMWRKNQVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
QY 121 HAVFSAVAPVSGTGQTSAELEVRHSLVSFVVRIVPSPDWFVGVDSLDLDCGDRWREQA 180
DB 121 HAVFSAVAPVSGTGQTSAELEVRHSLVSFVVRIVPSPDWFVGVDSLDLDCGDRWREQA 180
QY 181 ALDLYPYDAGTDSGFTFSSPNFATIPQDTVTITSSPSHPANSFYYPRLKALPPIARVT 240
DB 181 ALDLYPYDAGTDSGFTFSSPNFATIPQDTVTITSSPSHPANSFYYPRLKALPPIARVT 240
QY 241 LVRLRQSPRAFIIPAPVLPSPRDNIEIVDSASVPETPLDCEVLSWSSWGLCGGHCRLGTSK 300
DB 241 LVRLRQSPRAFIIPAPVLPSPRDNIEIVDSASVPETPLDCEVLSWSSWGLCGGHCRLGTSK 300
QY 301 RTRVVRVQPNANGSPCPELEEEAECPDNCV 331
DB 301 RTRVVRVQPNANGSPCPELEEEAECPDNCV 331

RESULT 3

ABG61806

ID ABG61806 standard; protein; 331 AA.

XX ABG61806;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 18:59:18 ; Search time 63.5911 Seconds
(without alignments)
500.821 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
Sequence: 1 MENPSPAAALGKALCALLLA.....NGSPCELEBEAEVCVDPNCV 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|----------|---------------------|
| 1 | 462.5 | 26.3 | 807 | 2 A38152 | F-spondin - rat |
| 2 | 448.5 | 25.5 | 803 | 2 A47723 | F-spondin precursor |
| 3 | 401 | 22.8 | 805 | 2 T34212 | hypothetical prote |
| 4 | 122.5 | 7.0 | 741 | 2 I48694 | probable transcrip |
| 5 | 117.5 | 6.7 | 770 | 2 D89447 | protein F57C12.1 [|
| 6 | 112 | 6.4 | 772 | 2 A55004 | transcription fact |
| 7 | 108 | 6.1 | 123 | 2 S49108 | TRAP-C2 protein - |
| 8 | 107 | 6.1 | 808 | 2 T10171 | phospholipase D (E |
| 9 | 104.5 | 5.9 | 440 | 2 T24232 | hypothetical prote |
| 10 | 103 | 5.9 | 742 | 2 A49672 | transcription fact |
| 11 | 102 | 5.8 | 1251 | 2 A57293 | latent transformin |
| 12 | 100.5 | 5.7 | 810 | 2 D96566 | hypothetical prote |
| 13 | 100.5 | 5.7 | 2957 | 2 T33152 | hypothetical prote |
| 14 | 99.5 | 5.7 | 590 | 2 I46687 | complement compone |
| 15 | 99.5 | 5.7 | 724 | 2 A48569 | antigen Em100 - Ei |
| 16 | 99.5 | 5.7 | 812 | 2 T03859 | phospholipase D (E |
| 17 | 98 | 5.6 | 903 | 2 T00705 | N-chimerin homolog |
| 18 | 97.5 | 5.5 | 808 | 2 T04092 | phospholipase D (E |
| 19 | 97 | 5.5 | 534 | 2 T41081 | hypothetical prote |
| 20 | 97 | 5.5 | 1360 | 2 T33922 | hypothetical prote |
| 21 | 96.5 | 5.5 | 598 | 2 A57249 | beta-galactosidase |
| 22 | 96.5 | 5.5 | 712 | 2 A45638 | immunodominant mic |
| 23 | 96.5 | 5.5 | 812 | 2 T03402 | probable phospholi |
| 24 | 96.5 | 5.5 | 912 | 2 A54423 | brevicin precursor |
| 25 | 96.5 | 5.5 | 1572 | 2 T00027 | brain-specific ang |
| 26 | 96 | 5.5 | 591 | 1 C8HUB | complement C8 beta |
| 27 | 96 | 5.5 | 1584 | 2 T00026 | brain-specific ang |
| 28 | 94 | 5.3 | 809 | 2 T11695 | phospholipase D (E |
| 29 | 93 | 5.3 | 483 | 1 VCBP13 | minor coat protein |

| | | | | | |
|----|------|-----|------|----------|--------------------|
| 30 | 92 | 5.2 | 1306 | 2 S25370 | MSB2 protein - Yea |
| 31 | 91.5 | 5.2 | 424 | 2 C70651 | hypothetical prote |
| 32 | 91 | 5.2 | 152 | 2 D89753 | protein Fl1C7.2 [1 |
| 33 | 91 | 5.2 | 862 | 2 T46289 | hypothetical prote |
| 34 | 91 | 5.2 | 937 | 2 D87483 | ribonucleotide red |
| 35 | 90 | 5.1 | 497 | 2 T41015 | proline rich prote |
| 36 | 90 | 5.1 | 692 | 2 AD1857 | hypothetical prote |
| 37 | 90 | 5.1 | 1444 | 2 T18856 | angiogenesis inhib |
| 38 | 90 | 5.1 | 1666 | 2 T43169 | hypothetical prote |
| 39 | 90 | 5.1 | 2265 | 1 FNBO | fibronectin - bovi |
| 40 | 90 | 5.1 | 3027 | 2 JQ1917 | polyprotein - pars |
| 41 | 89.5 | 5.1 | 919 | 2 T32541 | unc-5 protein - Ca |
| 42 | 89.5 | 5.1 | 947 | 1 B44294 | unc-5 protein, lon |
| 43 | 89 | 5.1 | 649 | 2 D96025 | probable adenylate |
| 44 | 89 | 5.1 | 697 | 2 T03834 | nuclear distributi |
| 45 | 89 | 5.1 | 1257 | 2 T09493 | period protein hom |

ALIGNMENTS

RESULT 1

A38152

F-spondin - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A38152

R:Klar, A.; Baldassare, M.; Jessell, T.M.

Cell 69, 95-110, 1992

A:Title: F-spondin: a gene expressed at high levels in the floor plate encodes a secretor

A:Reference number: A38152; MUID:92208952; PMID:1555244

A:Accession: A38152

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-807 <KLA>

A:Cross-references: UNIPROT:P35446; GB:M8469; NID:G204176; PIDN:AAA41174.1; PID:G204177

A:Experimental source: embryo floor plate

C:Note: sequence extracted from NCBI backbone (NCBIN:90877, NCBIP:90878)

C:Superfamily: F-spondin; thrombospondin type 1 repeat homology

F;441-495/Domain: thrombospondin type 1 repeat homology <THR2>

F;500-555/Domain: thrombospondin type 1 repeat homology <THR3>

F;557-611/Domain: thrombospondin type 1 repeat homology <THR4>

F;613-666/Domain: thrombospondin type 1 repeat homology <THR1>

F;667-721/Domain: thrombospondin type 1 repeat homology <THR5>

F;753-807/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 26.3%; Score 462.5; DB 2; Length 807;

Best Local Similarity 34.2%; Pred. No. 1.6e-28;

Matches 116; Conservative 49; Mismatches 137; Indels 37; Gaps 12;

QY 9 ALGKALCALLLATLGAAGPLGSESTCSAGAPAKYISITFTGKWSQTAFPKQYPLFRPPAQ 68

Db 176 SLTKKLCEQDPTLDGVTDTRPI---LDCCACGTAKYRLTFYGNWSEKTHPKDYP--RRANH 230

QY 69 WSLLLGAHSSDYSMRKKNQYVNSGLRDFAEERGEALMKEI-EAAGEALQSVHAFSAP 127

Db 231 WSAIIGSHSKNYLVMEYGGYASEGVKQVAELGSPVKMEETIRQQSDDEVLTUTVTKAKQWP 290

QY 128 -----AVPSGTGTSAELEVQRHSLVSFVVRIVPSPDWFEVSDSLDCLDGD-RWRE 178

Db 291 SWQPVNVRAP-----SAEFSVDRTHLSFLTMWGFSDNNVGLSAEDLCTKECGWVQ 344

QY 179 QAALDLYPYDAGTDSGFTSSNFATIPQDVTVEITSSPSHPANFYPRLLKALPIAR 238

Db 345 KVVQDLIPWDAGTDSGVTVESPNKPTIPEKIRPLTSL--DHPQSPFYDPEGGSITQVAR 402

QY 239 VTLVRL-RQSPRAFIPAPVLPSPRDNIEVDSASVPE-----TPLDCEVLSWSGLCGG 291

Db 403 VVIERIARKEQCNIYIPDNV---DDIVADLA--PEEKEDDDTPTETCIYSNWSFWSACSS 456

QY 292 HCGRLGTGKSTRVVRVQPPANNNGSPCELEBEAEVCVDPNC 330

Db 457 STCEKGRMRQRMKLAQ-LDLSVPCFDTQDFQFCMGPGC 494

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 18:51:02 ; Search time 308.988 Seconds
(without alignments)
548.560 Million cell updates/sec

Title: US-10-616-279-2
Perfect score: 1760
Sequence: 1 MENPSPAAALGKALCALLA.....NGSPCELEBAECVDPNCV 331

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | % | Query | Length | DB | ID | Description |
|------------|--------|-------|---|------------|--------|----|------------|--------------------|
| 1 | 1744 | 99.1 | | SPO2_HUMAN | 331 | 1 | SPO2_HUMAN | Q9bud6 homo sapien |
| 2 | 1506.5 | 85.6 | | SPO2_RAT | 330 | 1 | SPO2_RAT | Q9w775 rattus norv |
| 3 | 1494.5 | 84.9 | | SPO2_MOUSE | 330 | 1 | SPO2_MOUSE | Q8bms2 mus musculu |
| 4 | 1488.5 | 84.6 | | Q8VD28 | 330 | 2 | Q8VD28 | Q8vd28 mus musculu |
| 5 | 1403 | 79.7 | | Q6KAS6 | 289 | 2 | Q6KAS6 | Q6kas6 mus musculu |
| 6 | 1113.5 | 63.3 | | Q6DCM4 | 313 | 2 | Q6DCM4 | Q6dcm4 xenopus lae |
| 7 | 1108 | 63.0 | | Q42112 | 331 | 2 | Q42112 | Q42112 brachydanio |
| 8 | 871 | 49.5 | | Q42111 | 334 | 2 | Q42111 | Q42111 brachydanio |
| 9 | 522.5 | 29.7 | | Q9V746 | 601 | 2 | Q9V746 | Q9v746 drosophila |
| 10 | 512 | 29.1 | | Q02029 | 598 | 2 | Q02029 | Q02029 drosophila |
| 11 | 470.5 | 26.7 | | Q42113 | 808 | 2 | Q42113 | Q42113 brachydanio |
| 12 | 466 | 26.5 | | Q69Z27 | 729 | 2 | Q69Z27 | Q69z27 mus musculu |
| 13 | 464.5 | 26.4 | | SPO1_CHICK | 802 | 1 | SPO1_CHICK | Q9w770 gallus gall |
| 14 | 462.5 | 26.3 | | SPO1_MOUSE | 807 | 1 | SPO1_MOUSE | Q8vcc9 mus musculu |
| 15 | 462.5 | 26.3 | | SPO1_RAT | 807 | 1 | SPO1_RAT | P35446 rattus norv |
| 16 | 460.5 | 26.2 | | SPO1_BOVIN | 807 | 1 | SPO1_BOVIN | Q9glx9 bos taurus |
| 17 | 460.5 | 26.2 | | SPO1_HUMAN | 807 | 1 | SPO1_HUMAN | Q9hcb6 homo sapien |
| 18 | 457 | 26.0 | | Q76822 | 898 | 2 | Q76822 | Q76822 brachydanio |
| 19 | 448.5 | 25.5 | | SPO1_XENLA | 803 | 1 | SPO1_XENLA | P35447 xenopus lae |
| 20 | 447 | 25.4 | | Q7KR54 | 628 | 2 | Q7KR54 | Q7kr54 drosophila |
| 21 | 447 | 25.4 | | Q9XZD0 | 763 | 2 | Q9XZD0 | Q9xzd0 drosophila |
| 22 | 443 | 25.2 | | Q42114 | 803 | 2 | Q42114 | Q42114 brachydanio |
| 23 | 441.5 | 25.1 | | Q7KR42 | 873 | 2 | Q7KR42 | Q7kr42 drosophila |
| 24 | 440.5 | 25.0 | | Q7Q082 | 951 | 2 | Q7Q082 | Q7q082 anopheles g |
| 25 | 436 | 24.8 | | Q7PZ75 | 608 | 2 | Q7PZ75 | Q7pz75 anopheles g |
| 26 | 424.5 | 24.1 | | Q8ML26 | 839 | 2 | Q8ML26 | Q8ml26 drosophila |
| 27 | 420.5 | 23.9 | | Q9H711 | 216 | 2 | Q9H711 | Q9h711 homo sapien |
| 28 | 401 | 22.8 | | Q19305 | 819 | 2 | Q19305 | Q19305 caenorhabdi |
| 29 | 306 | 17.4 | | Q8ML27 | 861 | 2 | Q8ML27 | Q8ml27 drosophila |
| 30 | 280.5 | 15.9 | | Q8T988 | 549 | 2 | Q8T988 | Q8t988 drosophila |
| 31 | 271.5 | 15.4 | | Q95822 | 461 | 2 | Q95822 | Q95822 drosophila |

32 225.5 12.8 92 2 Q6DC15
33 149.5 8.5 1107 2 Q8BHP3
34 149 8.5 1607 2 Q6P4U0
35 144.5 8.2 1536 2 Q9C014
36 140.5 8.0 238 2 Q69HT6
37 134 7.6 1502 2 Q9UPZ6
38 134 7.6 1668 2 Q69ZU6
39 131 7.4 856 2 Q86PQ8
40 130 7.4 3869 2 Q86PQ3
41 128 7.3 687 2 Q23729
42 127 7.2 921 2 Q969A3
43 125 7.1 660 2 Q23832
44 123 7.0 243 2 Q8BFU0
45 122.5 7.0 437 2 Q7YF59

ALIGNMENTS

RESULT 1

SPO2_HUMAN STANDARD; PRT; 331 AA.
AC Q9BUD6; Q9ULW1;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DE Spondin 2 precursor (Madin) (Differentially expressed in cancerous and noncancerous lung cells 1) (DIL-1) (UNQ435/PRO866).
GN Name=SPO2; Synonyms=DIL1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND VARIANTS ALA-122 AND VAL-242.
RX MEDLINE=99443867; PubMed=10512675; DOI=10.1006/geno.1999.5939;
RA Manda R., Kohno T., Matsuno Y., Takenoshita S., Kuwano H., Yokota J.;
RT "Identification of genes (SPON2 and C20orf2) differentially expressed between cancerous and noncancerous lung cells by mRNA differential display.";
RL Genomics 61:5-14 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu O., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P., Gray A.;
RT "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment.";
RL Genomics Res. 13:2265-2270 (2003).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS ALA-122 AND VAL-242.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosono T., Kaku Y., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hirakawa S., Chiba T.,
RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N., Mueashino K., Yuiki H., Oshima A., Sasaki N., Aotsuka S., Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S., Moriya S., Momiya H., Satoh N., Takami S., Terashima Y., Suzuki O., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B., Yamazaki M., Watanabe K., Tsumagari A., Itakura S., Fukuzumi Y., Fujimori Y., Koniya M., Kamigaito H., Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Kawabata A., Hikiji T., Kobatake N., Inagaki H., Okamoto S., Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M., Togaishi T., Oyama M., Hata H., Watanabe M., Komatsu T., Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K., Okumura K., Nagase T., Nomura N., Kikuchi H., Masuno Y., Yamashita R., Nakai K., Iada I., Nakamura Y., Ohara O., Isogai T., Sugano S.; "Complete sequencing and characterization of 21,243 full-length human cDNAs.";

RL Nat. Genet. 36:40-45(2004).

RT [4]

RN SEQUENCE FROM N.A.

RP TISSUE=Colon, and Placenta;

RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Stapleton M., Narusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Rana S.S., McQuellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.N., Krzywicki M.I., Skalska U., Smalls D.E., Smercher A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

CC -!- FUNCTION: Cell adhesion protein that promotes adhesion and outgrowth of hippocampal embryonic neurons. Binds directly to bacteria and their components and functions as an opsonin for macrophage phagocytosis of bacteria. Essential in the initiation of the innate immune response and represents a unique pattern-recognition molecule in the ECM for microbial pathogens (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted. Extracellular matrix (By similarity).

CC -!- TISSUE SPECIFICITY: Expressed in normal lung tissues but not in lung carcinoma cell lines.

CC -!- SIMILARITY: Contains 1 spondin domain.

CC -!- SIMILARITY: Contains 1 TSP type-1 domain.

CC -----

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CC -----

CC EMBL; AB027466; BAA85892.1; -

CC EMBL; AY358948; AAQ89307.1; -

CC EMBL; AK074618; BAC11092.1; -

CC EMBL; AK074770; BAC11196.1; -

CC EMBL; BC027070; AAH02707.1; -

CC EMBL; BC036341; AAH36341.1; -

CC Genbank; HGNC:11253; SPON2.

CC H-InvDB; HIX0004013; -.

DR MIM; 605918; -.

DR InterPro; IPR009465; Spond N.

DR InterPro; IPR000884; TSP1.

DR Pfam; PF06468; Spond N; 1.

DR Pfam; PF00090; TSP 1; 1.

DR PROSITE; PS1020; SPONDIN; 1.

DR PROSITE; PS0092; TSP1; 1.

KW Cell adhesion; Extracellular matrix; Immune response; Polymorphism;

KW Signal.

FT SIGNAL. 1 26 Potential.

FT CHAIN 27 331 Spondin 2.

FT DOMAIN 31 221 Spondin.

FT VARIANT 40 40 TSP type-1.

FT VARIANT 122 122 P -> L (in dbSNP:922697).

FT VARIANT 242 242 E -> A (in dbSNP:11247975).

FT VARIANT 242 242 L -> V (in dbSNP:2279279).

FT VARIANT 242 242 L -> V (in dbSNP:019702).

FT VARIANT 242 242 L -> V (in dbSNP:019703).

FT SEQUENCE 331 AA; 35844 MW; 418E244B893C59F4 CRC64;

Query Match 99.1%; Score 1744; DB 1; Length 331;

Best Local Similarity 99.1%; Pred. No. 2.5e-128;

Matches 328; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MENPSPAAALGKALCALLLTLGAAGQPLGSGICSGAGAPAKYVITFTGKWSQTAFPKQY 60

DB 1 MENPSPAAALGKALCALLLTLGAAGQPLGSGICSGARAPAKYVITFTGKWSQTAFPKQY 60

QY 61 PLFRPPAOWSSLLGAHSSDYSMWRKQYVNSGLRDPFAERGEAWALMKEIEAAGALQSV 120

DB 61 PLFRPPAOWSSLLGAHSSDYSMWRKQYVNSGLRDPFAERGEAWALMKEIEAAGALQSV 120

QY 121 HAVFSAPAVPSGTGTGTSAELEVRHSLVSVFVYRIVPSDPWFVGVDSLDLDCDGRWRQQA 180

DB 121 HEVFSAPAVPSGTGTGTSAELEVRHSLVSVFVYRIVPSDPWFVGVDSLDLDCDGRWRQQA 180

QY 181 ALDLPYDAGTDSGTFTSSPNFATIPQDVTTEITSSSPSPHANSFYPRLKALPPIARVT 240

DB 181 ALDLPYDAGTDSGTFTSSPNFATIPQDVTTEITSSSPSPHANSFYPRLKALPPIARVT 240

QY 241 LVRLQSPRAFTIPAPVLPSPDNEIVDSASVPTPLDCEVLSWSSWGLCGHCGRLGTS 300

DB 241 LVRLQSPRAFTIPAPVLPSPDNEIVDSASVPTPLDCEVLSWSSWGLCGHCGRLGTS 300

QY 301 RTRYVRVOPANNQSPCELEBEEACVPDNCV 331

DB 301 RTRYVRVOPANNQSPCELEBEEACVPDNCV 331

RESULT 2

SPO2 RAT

ID SPO2 RAT STANDARD; PRT; 330 AA.

AC Q9W75;

DT 25-OCT-2004 (Rel. 45, Created)

DT 25-OCT-2004 (Rel. 45, Last sequence update)

DT 25-JAN-2005 (Rel. 46, Last annotation update)

DE Spondin 2 precursor (Mandarin).

GN Names=Spond2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.; FUNCTION, AND TISSUE SPECIFICITY.

RC STRAIN=Sprague-Dawley;

RX MEDLINE=99339921; PubMed=10409509;

RX Feinstein Y., Borrell V., Garcia C., Burstyn-Cohen T., Tzarfaty V., Frumkin A., Nose A., Okamoto H., Higashijima S., Soriano A., Klar A.; "P-spondin and mindin: two structurally and functionally related genes expressed in the hippocampus that promote outgrowth of embryonic hippocampal neurons.";

RT Development 126:3637-3648 (1999).

RL

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 14, 2005, 19:00:53 ; Search time 90.4951 Seconds
(without alignments)
273.041 Million cell updates/sec

Title: US-10-616-279-2

Perfect score: 1760

Sequence: 1 MENPSPAALGKALCALLA.....NGSPCELEAEACVDPNCV 331

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
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- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|---------------------|
| 1 | 1760 | 100.0 | 331 | 4 | US-09-732-357B-2 |
| 2 | 1742 | 99.0 | 331 | 2 | US-08-799-173A-2 |
| 3 | 1742 | 99.0 | 331 | 4 | US-09-170-042A-2 |
| 4 | 1551.5 | 88.2 | 330 | 3 | US-09-371-696-2 |
| 5 | 1506.5 | 85.6 | 330 | 4 | US-09-732-357B-13 |
| 6 | 1101.5 | 62.6 | 299 | 4 | US-09-311-021-202 |
| 7 | 464.5 | 26.4 | 802 | 1 | US-07-862-021B-12 |
| 8 | 464.5 | 26.4 | 802 | 1 | US-08-313-288B-12 |
| 9 | 464.5 | 26.4 | 802 | 5 | PCT-US93-03164-12 |
| 10 | 462.5 | 26.3 | 392 | 2 | US-08-799-173A-7 |
| 11 | 462.5 | 26.3 | 392 | 4 | US-09-170-042A-7 |
| 12 | 462.5 | 26.3 | 807 | 1 | US-07-862-021B-10 |
| 13 | 462.5 | 26.3 | 807 | 1 | US-08-313-288B-10 |
| 14 | 462.5 | 26.3 | 807 | 4 | US-09-132-769-5 |
| 15 | 462.5 | 26.3 | 807 | 5 | PCT-US93-03164-10 |
| 16 | 460.5 | 26.2 | 787 | 4 | US-09-825-294-207 |
| 17 | 460.5 | 26.2 | 787 | 4 | US-09-970-966-207 |
| 18 | 460.5 | 26.2 | 807 | 4 | US-09-132-769-1 |
| 19 | 460.5 | 26.2 | 807 | 4 | US-09-132-769-3 |
| 20 | 460.5 | 26.2 | 807 | 4 | US-09-640-173-186 |
| 21 | 460.5 | 26.2 | 807 | 4 | US-09-713-550-186 |
| 22 | 460.5 | 26.2 | 807 | 4 | US-09-825-294-186 |
| 23 | 460.5 | 26.2 | 807 | 4 | US-09-970-966-186 |
| 24 | 438.5 | 24.9 | 819 | 4 | US-09-270-767-42963 |
| 25 | 422.5 | 24.0 | 677 | 4 | US-09-270-767-58094 |
| 26 | 422.5 | 24.0 | 847 | 4 | US-09-270-767-42783 |
| 27 | 420.5 | 23.9 | 132 | 3 | US-09-022-238-2 |

| | | | | | | |
|----|-------|------|-----|---|---------------------|-------------------|
| 28 | 331 | 18.8 | 568 | 1 | US-07-862-021B-14 | Sequence 14, Appl |
| 29 | 331 | 18.8 | 568 | 5 | PCT-US93-03164-14 | Sequence 14, Appl |
| 30 | 309 | 17.6 | 53 | 2 | US-08-799-173A-18 | Sequence 18, Appl |
| 31 | 309 | 17.6 | 53 | 4 | US-09-170-042A-19 | Sequence 19, Appl |
| 32 | 189 | 10.7 | 37 | 3 | US-09-022-238-3 | Sequence 3, Appli |
| 33 | 181 | 10.3 | 37 | 3 | US-09-371-696-3 | Sequence 3, Appli |
| 34 | 130.5 | 7.4 | 56 | 1 | US-07-862-021B-19 | Sequence 19, Appl |
| 35 | 130.5 | 7.4 | 56 | 5 | PCT-US93-03164-19 | Sequence 19, Appl |
| 36 | 128.5 | 7.3 | 50 | 2 | US-08-799-173A-14 | Sequence 14, Appl |
| 37 | 128.5 | 7.3 | 50 | 4 | US-09-170-042A-14 | Sequence 14, Appl |
| 38 | 121.5 | 6.9 | 52 | 2 | US-08-799-173A-12 | Sequence 12, Appl |
| 39 | 121.5 | 6.9 | 52 | 4 | US-09-170-042A-12 | Sequence 12, Appl |
| 40 | 116 | 6.6 | 23 | 4 | US-09-732-357B-11 | Sequence 11, Appl |
| 41 | 110.5 | 6.3 | 149 | 4 | US-09-270-767-32202 | Sequence 32202, A |
| 42 | 110.5 | 6.3 | 149 | 4 | US-09-270-767-47419 | Sequence 47419, A |
| 43 | 108 | 6.1 | 19 | 4 | US-09-732-357B-9 | Sequence 9, Appli |
| 44 | 103 | 5.9 | 229 | 4 | US-09-894-912A-25 | Sequence 25, Appl |
| 45 | 101 | 5.7 | 160 | 4 | US-09-894-912A-14 | Sequence 14, Appl |

ALIGNMENTS

RESULT 1

US-09-732-357B-2
; Sequence 2, Application US/09732357B
; Patent No. 6682902
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. 6682902el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSM1
; CURRENT APPLICATION NUMBER: US/09/732,357B
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-732-357B-2

| | | | | |
|-----------------------|-----------------|--|---------------|-------------|
| Query Match | 100.0%; | Score 1760; | DB 4; | Length 331; |
| Best Local Similarity | 100.0%; | Pred. No. 8.2e-166; | Mismatches 0; | Indels 0; |
| Matches 331; | Conservative 0; | | | Gaps 0; |
| QY | 1 | MENPSPAALGKALCALLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSOTAFPKQY | 60 | |
| Db | 1 | MENPSPAALGKALCALLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSOTAFPKQY | 60 | |
| QY | 61 | PLFRPPAQWSSLLGAHSSDYSMWRKXQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV | 120 | |
| Db | 61 | PLFRPPAQWSSLLGAHSSDYSMWRKXQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV | 120 | |
| QY | 121 | HAVFSAAPVPSGGTSAELEVQRHSLVSFVVRIVPSDFWGVDSLDLDCGDRWEQA | 180 | |
| Db | 121 | HAVFSAAPVPSGGTSAELEVQRHSLVSFVVRIVPSDFWGVDSLDLDCGDRWEQA | 180 | |
| QY | 181 | ALDLYPYDAGTDSGFTFSSPNFATIPQDTVTEITSSPSHPANSFYYPRLKALPPIARVT | 240 | |
| Db | 181 | ALDLYPYDAGTDSGFTFSSPNFATIPQDTVTEITSSPSHPANSFYYPRLKALPPIARVT | 240 | |
| QY | 241 | LVLRLQSPRAFIAPPVLPVPSRDNIEVDASVPETPLDCEVSLWSSWGLCGHCGRLGTKS | 300 | |
| Db | 241 | LVLRLQSPRAFIAPPVLPVPSRDNIEVDASVPETPLDCEVSLWSSWGLCGHCGRLGTKS | 300 | |
| QY | 301 | RTFYVQVPPANNSSPCPELEAEACVDPNCV | 331 | |
| Db | 301 | RTFYVQVPPANNSSPCPELEAEACVDPNCV | 331 | |

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RESULT 2
US-08-799-173A-2
; Sequence 2, Application US/08799173A
; Patent No. 5871969
; GENERAL INFORMATION:
; APPLICANT: HASTINGS, GREGG,
; APPLICANT: PATRICK J. DILLON
; TITLE OF INVENTION: HUMAN NEURONAL ATTACHMENT FACTOR-1
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF226
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 331 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-799-173A-2

Query Match      99.0%; Score 1742; DB 2; Length 331;
Best Local Similarity 99.4%; Pred. No. 5e-164;
Matches 329; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MENPSAAALGKALCALLATLGAAGQPLGGESICSA GAPAKYSITFTGKWSQTAPPKQY 60
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Db      1 MENPSAAALGKALCALLATLGAAGQPLGGESICSA RALAKYSITFTGKWSQTAPPKQY 60
      |||

QY      61 PLFRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
      |||
Db      61 PLFRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
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QY      121 HAVFSAPAVPSGTGQTSAELEVQRHSLVSFVVRIVPSDPWFVGVDSLDLDCGDRWREQA 180
      |||
Db      121 HAVFSAPAVPSGTGQTSAELEVQRHSLVSFVVRIVPSDPWFVGVDSLDLDCGDRWREQA 180
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QY      181 ALDLYPYDAGTDSGFTFSSPNFATIPQDVTTEITSSPSHPANSFYYPRLKALPPIARVT 240
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QY      241 LVLRQSPRAFI PPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGHCGRLGTSK 300
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Db      241 LVLRQSPRAFI PPAPVLP SRDNEIVDSASVPETPLDCEVSLWSSWGLCGHCGRLGTSK 300
      |||

QY      301 RTRVVRVQPNNGSPCPPELEEEAEACVPDNCV 331
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Db      301 RTRVVRVQPNNGSPCPPELEEEAEACVPDNCV 331
      |||

RESULT 4
US-09-371-696-2
; Sequence 2, Application US/09371696
; Patent No. 6287777
; GENERAL INFORMATION:
; APPLICANT: Sytkowski, Arthur J.
; APPLICANT: Yang, Meiheng
; TITLE OF INVENTION: NOVEL NFG-1 GENE THAT IS DIFFERENTIALLY EXPRESSED IN PROSTATE
; FILE OF INVENTION: TUMORS
; FILE REFERENCE: 01948/053002
; CURRENT APPLICATION NUMBER: US/09/371,696
; CURRENT FILING DATE: 1999-08-10
; EARLIER APPLICATION NUMBER: US 09/022,238
; EARLIER FILING DATE: 1998-02-11
; EARLIER APPLICATION NUMBER: US 08/644,326
; EARLIER FILING DATE: 1996-05-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-371-696-2

Query Match      88.2%; Score 1551.5; DB 3; Length 330;
Best Local Similarity 87.6%; Pred. No. 3.6e-145;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 14, 2005, 19:11:14 ; Search time 317.14 Seconds
(without alignments)
436.695 Million cell updates/sec

Title: US-10-616-279-2

Perfect score: 1760

Sequence: 1 MENPSPAALGKALCALLLA.....NGSPCELEBEEACVDPNCV 331

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2 | 1760 | 100.0 | 331 | 15 | US-10-616-279-2 |
| 3 | 1760 | 100.0 | 331 | 16 | US-10-624-884-2 |
| 4 | 1760 | 100.0 | 331 | 17 | US-10-895-183-2 |
| 5 | 1752 | 99.5 | 331 | 10 | US-09-970-944-12 |
| 6 | 1752 | 99.5 | 331 | 10 | US-09-970-944-38 |
| 7 | 1752 | 99.5 | 331 | 14 | US-10-205-823-385 |
| 8 | 1752 | 99.5 | 331 | 15 | US-10-295-027-132 |
| 9 | 1752 | 99.5 | 331 | 15 | US-10-295-027-1195 |
| 10 | 1752 | 99.5 | 331 | 16 | US-10-723-860-1632 |
| 11 | 1752 | 99.5 | 331 | 18 | US-10-631-467-907 |

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| 12 | 1752 | 99.5 | 331 | 20 | US-11-051-454-385 |
| 13 | 1747 | 99.3 | 331 | 18 | US-10-929-973-2 |
| 14 | 1747 | 99.3 | 349 | 18 | US-10-919-215-1 |
| 15 | 1744 | 99.1 | 331 | 9 | US-09-978-295A-236 |
| 16 | 1744 | 99.1 | 331 | 9 | US-09-938-418-8 |
| 17 | 1744 | 99.1 | 331 | 9 | US-09-978-697-236 |
| 18 | 1744 | 99.1 | 331 | 9 | US-09-978-192A-236 |
| 19 | 1744 | 99.1 | 331 | 9 | US-09-999-832A-236 |
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| 24 | 1744 | 99.1 | 331 | 10 | US-09-978-403A-236 |
| 25 | 1744 | 99.1 | 331 | 10 | US-09-978-564A-236 |
| 26 | 1744 | 99.1 | 331 | 10 | US-09-999-833A-236 |
| 27 | 1744 | 99.1 | 331 | 10 | US-09-981-915A-236 |
| 28 | 1744 | 99.1 | 331 | 10 | US-09-978-824-236 |
| 29 | 1744 | 99.1 | 331 | 10 | US-09-918-585A-236 |
| 30 | 1744 | 99.1 | 331 | 10 | US-09-999-834A-236 |
| 31 | 1744 | 99.1 | 331 | 10 | US-09-978-423A-236 |
| 32 | 1744 | 99.1 | 331 | 10 | US-09-978-193A-236 |
| 33 | 1744 | 99.1 | 331 | 10 | US-09-999-830A-236 |
| 34 | 1744 | 99.1 | 331 | 10 | US-09-978-757A-236 |
| 35 | 1744 | 99.1 | 331 | 10 | US-09-978-187B-236 |
| 36 | 1744 | 99.1 | 331 | 10 | US-09-978-643A-236 |
| 37 | 1744 | 99.1 | 331 | 10 | US-09-978-375A-236 |
| 38 | 1744 | 99.1 | 331 | 10 | US-09-978-298A-236 |
| 39 | 1744 | 99.1 | 331 | 10 | US-09-978-188A-236 |
| 40 | 1744 | 99.1 | 331 | 10 | US-09-978-681A-236 |
| 41 | 1744 | 99.1 | 331 | 10 | US-09-978-194A-236 |
| 42 | 1744 | 99.1 | 331 | 10 | US-09-999-829A-236 |
| 43 | 1744 | 99.1 | 331 | 10 | US-09-978-299A-236 |
| 44 | 1744 | 99.1 | 331 | 10 | US-09-978-544A-236 |
| 45 | 1744 | 99.1 | 331 | 10 | US-09-978-665A-236 |

ALIGNMENTS

RESULT 1

US-09-732-357A-2

; Sequence 2, Application US/09732357A

; Patent No. US20020004047A1

; GENERAL INFORMATION:

; APPLICANT: Harkins, Richard

; APPLICANT: Parkes, Deborah

; APPLICANT: Barry, Gordon

; APPLICANT: Schneider, Douglas

; APPLICANT: Steindbrecher, Renate

; TITLE OF INVENTION: DNA Encoding a No. US20020004047A1el RG-1 Polypeptide

; FILE REFERENCE: 51791AUSM1

; CURRENT APPLICATION NUMBER: US/09/732,357A

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: 60/172,370

; PRIOR FILING DATE: 1999-12-16

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 331

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-732-357A-2

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| Best Local Similarity | 100.0%; | Pred. No. 1.6e-150; | | |
| Matches 331; | Conservative | 0; | Mismatches | 0; |
| Indels | 0; | Gaps | 0; | |
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| Db | 1 | MENPSPAALGKALCALLLATLGAAGQPLGSGESCSAGAPAKYSITFTGKWSQTAFPKQY | 60 | |
| Qy | 61 | PLRFPAPQWSLLGAHSSDYSMWKQYVNSGLRDFAEERGEAWALKEITAEAGNLSV | 120 | |

Db 61 PLFRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
Qy 121 HAVFSAFAPVSGTGTSAELEVORRHSLVSFVVRIVSPDMFVGVDSLDLDCDGRWREQA 180
Db 121 HAVFSAFAPVSGTGTSAELEVORRHSLVSFVVRIVSPDMFVGVDSLDLDCDGRWREQA 180
Qy 181 ALDLYPDAGTDSGTFSSPNFATIPQDTVTETITSSSPSHPANSFYPRKALPPIARVT 240
Db 181 ALDLYPDAGTDSGTFSSPNFATIPQDTVTETITSSSPSHPANSFYPRKALPPIARVT 240
Qy 241 LVRLQSPRAFIIPAPVLPSPRNEIVDSASVPETPLDCEVLSWSSWGLCGHCGRLGTSK 300
Db 241 LVRLQSPRAFIIPAPVLPSPRNEIVDSASVPETPLDCEVLSWSSWGLCGHCGRLGTSK 300
Qy 301 RTRVVRVQPNNGSPCPPELEEEAEACVPDNCV 331
Db 301 RTRVVRVQPNNGSPCPPELEEEAEACVPDNCV 331

RESULT 2

US-10-616-279-2
; Sequence 2, Application US/10616279
; Publication No. US20040023307A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a No. US20040023307A1el RG-1 Polypeptide
; FILE REFERENCE: 51791AUSD1
; CURRENT APPLICATION NUMBER: US/10/616,279
; PRIOR FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-616-279-2

Query Match 100.0%; Score 1760; DB 15; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.6e-150;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MENPSPAAALGKALCALLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSQTAPPKQY 60
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Db 61 PLFRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
Qy 121 HAVFSAFAPVSGTGTSAELEVORRHSLVSFVVRIVSPDMFVGVDSLDLDCDGRWREQA 180
Db 121 HAVFSAFAPVSGTGTSAELEVORRHSLVSFVVRIVSPDMFVGVDSLDLDCDGRWREQA 180
Qy 181 ALDLYPDAGTDSGTFSSPNFATIPQDTVTETITSSSPSHPANSFYPRKALPPIARVT 240
Db 181 ALDLYPDAGTDSGTFSSPNFATIPQDTVTETITSSSPSHPANSFYPRKALPPIARVT 240
Qy 241 LVRLQSPRAFIIPAPVLPSPRNEIVDSASVPETPLDCEVLSWSSWGLCGHCGRLGTSK 300
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RESULT 3
US-10-624-884-2
; Sequence 2, Application US/10624884
; Publication No. US20040152139A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: DNA Encoding a Novel RG-1 Polypeptide
; FILE REFERENCE: 51791AUSC1
; CURRENT APPLICATION NUMBER: US/10/624,884
; PRIOR FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US 60/172,370
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/732,357
; PRIOR FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; TYPE: PRT
; LENGTH: 331
; ORGANISM: Homo sapiens
US-10-624-884-2
Query Match 100.0%; Score 1760; DB 16; Length 331;
Best Local Similarity 100.0%; Pred. No. 1.6e-150;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MENPSPAAALGKALCALLATLGAAGQPLGGESICSAGAPAKYSITFTGKWSQTAPPKQY 60
Qy 61 PLFRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
Db 61 PLFRPPAQWSSLLGAAHSSDYSMWRKNQYVNSGLRDFAEERGEAWALMKEIEAAGEALQSV 120
Qy 121 HAVFSAFAPVSGTGTSAELEVORRHSLVSFVVRIVSPDMFVGVDSLDLDCDGRWREQA 180
Db 121 HAVFSAFAPVSGTGTSAELEVORRHSLVSFVVRIVSPDMFVGVDSLDLDCDGRWREQA 180
Qy 181 ALDLYPDAGTDSGTFSSPNFATIPQDTVTETITSSSPSHPANSFYPRKALPPIARVT 240
Db 181 ALDLYPDAGTDSGTFSSPNFATIPQDTVTETITSSSPSHPANSFYPRKALPPIARVT 240
Qy 241 LVRLQSPRAFIIPAPVLPSPRNEIVDSASVPETPLDCEVLSWSSWGLCGHCGRLGTSK 300
Db 241 LVRLQSPRAFIIPAPVLPSPRNEIVDSASVPETPLDCEVLSWSSWGLCGHCGRLGTSK 300
Qy 301 RTRVVRVQPNNGSPCPPELEEEAEACVPDNCV 331
Db 301 RTRVVRVQPNNGSPCPPELEEEAEACVPDNCV 331

RESULT 4

US-10-895-183-2
; Sequence 2, Application US/10895183
; Publication No. US20050019845A1
; GENERAL INFORMATION:
; APPLICANT: Harkins, Richard
; APPLICANT: Parkes, Deborah
; APPLICANT: Parry, Gordon
; APPLICANT: Schneider, Douglas
; APPLICANT: Steinbrecher, Renate
; TITLE OF INVENTION: RG1 Antibodies and Uses Thereof
; FILE REFERENCE: 51791BUSM1
; CURRENT APPLICATION NUMBER: US/10/895,183
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 60/489,032
; PRIOR FILING DATE: 2003-07-22
; NUMBER OF SEQ ID NOS: 31